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## SEQUENCE LISTING

<110> BASF Plant Science GmbH  
SweTree Technologies AB

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<120> IMPROVED CONSTRUCTS FOR MARKER EXCISION BASED ON DUAL-FUNCTION  
SELECTION MARKER

10 <130> PF 55443 EP

<160> 16

<170> PatentIn version 3.1

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<212> DNA

<213> Rhodosporidium toruloides

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<222> (1)..(1104)

<223> coding for DAAO

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ctg agc agc gcc ctc atc ctc gct cgg aag ggc tac agc gtg cat att 96

Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile

20 25 30

35 ctc gcg cgc gac ttg ccg gag gac gtc tcg agc cag act ttc gct tca 144

Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser

35 40 45

cca tgg gct ggc gcg aat tgg acg cct ttc atg acg ctt aca gac ggt 192

40 Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly

50 55 60

oct cga caa gca aaa tgg gaa gaa tcg act ttc aag aag tgg gtc gag 240

Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu

45 65 70 75 80

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	Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe	
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5	gcg cag aac gaa gac ggc ttg ctc ggg cac tgg tac aag gac atc acg	336
	Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr	
	100 105 110	
10	cca aat tac cgc ccc ctc cca tct tcc gaa tgt cca cct ggc gct atc	384
	Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile	
	115 120 125	
15	ggc gta acc tac gac acc ctc tcc gtc cac gca cca aag tac tgc cag	432
	Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln	
	130 135 140	
20	tac ctt gca aga gag ctg cag aag ctc ggc gcg acg ttt gag aga cgg	480
	Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg	
	145 150 155 160	
25	acc gtt acg tcg ctt gag cag gcg ttc gac ggt gcg gat ttg gtg gtc	528
	Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val	
	165 170 175	
30	aac gct acg gga ctt ggc gcc aag tcg att gcg ggc atc gac gac caa	576
	Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln	
	180 185 190	
35	gcc gcc gag cca atc cgc ggg caa acc gtc ctc gtc aag tcc cca tgc	624
	Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys	
	195 200 205	
40	aag cga tgc acg atg gac tcg tcc gac ccc gct tct ccc gcc tac atc	672
	Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile	
	210 215 220	
45	att ccc cga cca ggt ggc gaa gtc atc tgc ggc ggg acg tac ggc gtg	720
	Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val	
	225 230 235 240	
50	gga gac tgg gac ttg tct gtc aac cca gag acg gtc cag cgg atc ctc	768
	Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu	
	245 250 255	

aag cac tgc ttg cgc ctc gac ccg acc atc tcg agc gac gga acg atc 816  
 Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile  
 260 265 270

5 gaa ggc atc gag gtc ctc cgc cac aac gtc ggc ttg cga cct gca cga 864  
 Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg  
 275 280 285

10 cga ggc gga ccc cgc gtt gag gca gaa cgg atc gtc ctg cct ctc gac 912  
 Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp  
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15 cgg aca aag tcg ccc ctc tcg ctc ggc agg ggc agc gca cga gcg gcg 960  
 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala  
 305 310 315 320

20 aag gag aag gag gtc acg ctt gtg cat gcg tat ggc ttc tcg agt gcg 1008  
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 325 330 335

gga tac cag cag agt tgg ggc gcg gcg gag gat gtc gcg cag ctc gtc 1056  
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 340 345 350

25 gac gag gcg ttc cag cgg tac cac ggc gcg gcg cgg gag tcg aag ttg 1104  
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45 Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser  
 35 40 45

Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly  
 50 55 60

5 Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu  
 65 70 75 80

Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe  
 85 90 95

10 Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr  
 100 105 110

15 Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile  
 115 120 125

Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln  
 130 135 140

20 Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg  
 145 150 155 160

Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val  
 165 170 175

25 Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln  
 180 185 190

Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys  
 195 200 205

30 Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile  
 210 215 220

35 Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val  
 225 230 235 240

Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu  
 245 250 255

40 Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile  
 260 265 270

45 Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg  
 275 280 285

Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp  
 290 295 300

5 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala  
 305 310 315 320

Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala  
 325 330 335

10 Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val  
 340 345 350

Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu  
 15 355 360 365

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 20 <213> *Caenorhabditis elegans*

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 <222> (1)..(1002)  
 25 <223> coding for DAAD

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gga tgt act tca gca ctt caa ata tca aaa gct ata cca aat gcg aaa 96  
 Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys  
 20 25 30

35 ata act gtg ctc cac gat aaa cca ttt aaa aaa tcg tgc agt gca gga 144  
 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly  
 35 40 45

40 cca gca gga tta ttt aga atc gat tat gag gag aat act gaa tac gga 192  
 Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly  
 50 55 60

cgt gct tct ttc gcc tgg ttc tca cat ctc tat cgc act aca aaa gga 240  
 45 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly

	65	70	75	80	
	tcc gaa acc ggc	gtg aaa tta gtt tct	gga cat att caa	tcc gac aac	288
	Ser Glu Thr Gly	Val Lys Leu Val	Ser Gly His Ile	Gln Ser Asp Asn	
5		85	90	95	
	ttg gag tca ttg	aag caa caa caa	aga gcc tat ggc	gat att gtg tac	336
	Leu Glu Ser Leu	Lys Gln Gln Gln	Arg Ala Tyr Gly	Asp Ile Val Tyr	
		100	105	110	
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	aac ttt aga ttc	ttg gat gat aga	gaa cgg ctg gac	att ttt ccc gaa	384
	Asn Phe Arg Phe	Leu Asp Asp Arg	Glu Arg Leu Asp	Ile Phe Pro Glu	
		115	120	125	
15					
	cca tca aag cac	tgc att cac tac	acc gcc tac gca	tca gaa ggt aac	432
	Pro Ser Lys His	Cys Ile His Tyr	Thr Ala Tyr Ala	Ser Glu Gly Asn	
		130	135	140	
	aag tac gtg cct	tat ttg aag aat	ttg ctg ctt gag	caa aaa atc gag	480
20	Lys Tyr Val Pro	Tyr Leu Lys Asn	Leu Leu Leu Glu	Gln Lys Ile Glu	
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	Phe Lys Gln Gln	Glu Val Thr Ser	Leu Asp Ala Val	Ala Asp Ala Gly	
25		165	170	175	
	tac gat gtt att	gta aac tgc gca	ggc ttg tac ggt	gga aag ttg gct	576
	Tyr Asp Val Ile	Val Asn Cys Ala	Gly Leu Tyr Gly	Gly Lys Leu Ala	
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	ggt gat gac gat	act tgc tac ccc	att aga gga gtc	att ttg gaa gtt	624
	Gly Asp Asp Asp	Thr Cys Tyr Pro	Ile Arg Gly Val	Ile Leu Glu Val	
		195	200	205	
35					
	gat gca cca tgg	cac aag cac ttc	aat tat cga gac	ttt act act ttc	672
	Asp Ala Pro Trp	His Lys His Phe	Asn Tyr Arg Asp	Phe Thr Thr Phe	
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	aca att cca aaa	gag cac agc gtg	gtg gtt ggg tcc	acc aag cag gac	720
40	Thr Ile Pro Lys	Glu His Ser Val	Val Val Gly Ser	Thr Lys Gln Asp	
		225	230	235	240
	aat cga tgg gat	ttg gag atc acc	gac gag gat aga	aat gat att ttg	768
45	Asn Arg Trp Asp	Leu Glu Ile Thr	Asp Glu Asp Arg	Asn Asp Ile Leu	
		245	250	255	

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 Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile  
 260 265 270

5 aaa gaa tgg tca gca ctt cgc ccg gga cgt aag cat gtc aga att gaa 864  
 Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu  
 275 280 285

10 gcg cag aag agg aca tct gtt gga aac tca aaa gat tat atg gtt gtg 912  
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 290 295 300

15 cat cac tat ggt cac ggg agc aac gga ttc acg ttg ggt tgg gga aca 960  
 His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr  
 305 310 315 320

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35 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly  
 35 40 45

Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly  
 50 55 60

40 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly  
 65 70 75 80

Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn  
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Leu Glu Ser Leu Lys Gln Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr  
 100 105 110

5 Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu  
 115 120 125

Pro Ser Lys His Cys Ile His Tyr Thr Ala Tyr Ala Ser Glu Gly Asn  
 130 135 140

10 Lys Tyr Val Pro Tyr Leu Lys Asn Leu Leu Leu Glu Gln Lys Ile Glu  
 145 150 155 160

Phe Lys Gln Gln Glu Val Thr Ser Leu Asp Ala Val Ala Asp Ala Gly  
 165 170 175

15 Tyr Asp Val Ile Val Asn Cys Ala Gly Leu Tyr Gly Gly Lys Leu Ala  
 180 185 190

Gly Asp Asp Asp Thr Cys Tyr Pro Ile Arg Gly Val Ile Leu Glu Val  
 20 195 200 205

Asp Ala Pro Trp His Lys His Phe Asn Tyr Arg Asp Phe Thr Thr Phe  
 210 215 220

25 Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp  
 225 230 235 240

Asn Arg Trp Asp Leu Glu Ile Thr Asp Glu Asp Arg Asn Asp Ile Leu  
 245 250 255

- 30 Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile  
 260 265 270

35 Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu  
 275 280 285

Ala Gln Lys Arg Thr Ser Val Gly Asn Ser Lys Asp Tyr Met Val Val  
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40 His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr  
 305 310 315 320

Ala Ile Glu Ala Thr Lys Leu Val Lys Thr Ala Leu Gly Leu  
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 Val Val Val Gly Ala Gly Val Ile Gly Leu Thr Ser Ala Leu Leu Leu  
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 tcc aag aac aag ggc aac aag atc acc gtc gtg gcc aag cac atg ccc 152  
 Ser Lys Asn Lys Gly Asn Lys Ile Thr Val Val Ala Lys His Met Pro  
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 ggc gac tat gac gtt gaa tac gcc tcg cct ttt gct ggt gcc aac cac 200  
 Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe Ala Gly Ala Asn His  
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 tcc ccc atg gcg acg gaa gag agc agc gaa tgg gaa cgt cgc act tgg 248  
 Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp Glu Arg Arg Thr Trp  
 55 60 65  
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 tac gag ttt aag aga ctg gtc gag gag gtc cct gag gcc ggt gtt cat 296  
 Tyr Glu Phe Lys Arg Leu Val Glu Glu Val Pro Glu Ala Gly Val His  
 70 75 80 85  
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 ttc cag aag tct cgc atc cag agg cgc aat gtg gac act gaa aag gcg 344  
 Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val Asp Thr Glu Lys Ala  
 90 95 100  
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 cag agg tct ggt ttc cca gac gcc ctc ttc tcg aaa gaa ccc tgg ttc 392  
 Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser Lys Glu Pro Trp Phe  
 105 110 115  
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 aag aac atg ttt gag gac ttc cgt gag cag cac cct agc gag gtc atc 440  
 Lys Asn Met Phe Glu Asp Phe Arg Glu Gln His Pro Ser Glu Val Ile

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	Pro Gly Tyr Asp Ser Gly Cys Glu Phe Thr Ser Val Cys Ile Asn Thr			
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	gcc atc tac ctc ccc tgg ctc ctc ggc cag tgc atc aag aat ggc gtc			536
	Ala Ile Tyr Leu Pro Trp Leu Leu Gly Gln Cys Ile Lys Asn Gly Val			
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	atc gtc aag cgc gcc atc ctc aac gac att agc gag gcc aag aag ctg			584
	Ile Val Lys Arg Ala Ile Leu Asn Asp Ile Ser Glu Ala Lys Lys Leu			
	170	175	180	
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	agc cac gcg ggc aag acg ccc aat atc atc gtc aac gcc acg ggt ctc			632
	Ser His Ala Gly Lys Thr Pro Asn Ile Ile Val Asn Ala Thr Gly Leu			
	185	190	195	
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20	Gly Ser Tyr Lys Leu Gly Gly Val Glu Asp Lys Thr Met Ala Pro Ala			
	200	205	210	
	cgg gga cag att gtg gtt gtg cgc aac gag agc agc ccc atg ctc ctc			728
	Arg Gly Gln Ile Val Val Val Arg Asn Glu Ser Ser Pro Met Leu Leu			
25	215	220	225	
	act tca ggt gtc gag gac ggc ggt gct gat gtc atg tac ttg atg cag			776
	Thr Ser Gly Val Glu Asp Gly Gly Ala Asp Val Met Tyr Leu Met Gln			
	230	235	240	245
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	cga gca gct ggc ggt ggc acc atc ctg ggc ggt acc tac gac gtt ggc			824
	Arg Ala Ala Gly Gly Gly Thr Ile Leu Gly Gly Thr Tyr Asp Val Gly			
	250	255	260	
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	aac tgg gag tct cag cca gac ccc aac atc gcg aat cgc atc atg cag			872
	Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala Asn Arg Ile Met Gln			
	265	270	275	
	cgc atc gtc gag gtg cgg ccc gag att gcc aac ggc aag ggc gtc aag			920
40	Arg Ile Val Glu Val Arg Pro Glu Ile Ala Asn Gly Lys Gly Val Lys			
	280	285	290	
	ggg ctg agc gtg atc cga cac gcc gtc ggc atg cgg ccg tgg cga aag			968
	Gly Leu Ser Val Ile Arg His Ala Val Gly Met Arg Pro Trp Arg Lys			
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gac gga gtc agg atc gag gag gag aag ctg gat gat gag act tgg atc 1016  
 Asp Gly Val Arg Ile Glu Glu Glu Lys Leu Asp Asp Glu Thr Trp Ile  
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 gtg cac aac tac gga cac tct gga tgg ggt tac cag ggt tcg tat ggt 1064  
 Val His Asn Tyr Gly His Ser Gly Trp Gly Tyr Gln Gly Ser Tyr Gly  
 330 335 340  
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 tgt gct gag aat gta gtc cag ttg gtt gac aag gtc ggc aag gcg gcc 1112  
 Cys Ala Glu Asn Val Val Gln Leu Val Asp Lys Val Gly Lys Ala Ala  
 345 350 355  
 aag tct aag ctg tagttgaaaa ggctgaatg agtaatagta attggatatt 1164  
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 Ala Lys His Met Pro Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe  
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 Ala Gly Ala Asn His Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp  
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 Glu Arg Arg Thr Trp Tyr Glu Phe Lys Arg Leu Val Glu Glu Val Pro  
 65 70 75 80  
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 Glu Ala Gly Val His Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val  
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 Asp Thr Glu Lys Ala Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser  
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Lys Glu Pro Trp Phe Lys Asn Met Phe Glu Asp Phe Arg Glu Gln His  
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5 Pro Ser Glu Val Ile Pro Gly Tyr Asp Ser Gly Cys Glu Phe Thr Ser  
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Val Cys Ile Asn Thr Ala Ile Tyr Leu Pro Trp Leu Leu Gly Gln Cys  
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10 Ile Lys Asn Gly Val Ile Val Lys Arg Ala Ile Leu Asn Asp Ile Ser  
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Glu Ala Lys Lys Leu Ser His Ala Gly Lys Thr Pro Asn Ile Ile Val  
 15 180 185 190

Asn Ala Thr Gly Leu Gly Ser Tyr Lys Leu Gly Gly Val Glu Asp Lys  
 195 200 205

20 Thr Met Ala Pro Ala Arg Gly Gln Ile Val Val Val Arg Asn Glu Ser  
 210 215 220

Ser Pro Met Leu Leu Thr Ser Gly Val Glu Asp Gly Gly Ala Asp Val  
 225 230 235 240

25 Met Tyr Leu Met Gln Arg Ala Ala Gly Gly Gly Thr Ile Leu Gly Gly  
 245 250 255

Thr Tyr Asp Val Gly Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala  
 30 260 265 270

Asn Arg Ile Met Gln Arg Ile Val Glu Val Arg Pro Glu Ile Ala Asn  
 275 280 285

35 Gly Lys Gly Val Lys Gly Leu Ser Val Ile Arg His Ala Val Gly Met  
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Arg Pro Trp Arg Lys Asp Gly Val Arg Ile Glu Glu Glu Lys Leu Asp  
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Asp Glu Thr Trp Ile Val His Asn Tyr Gly His Ser Gly Trp Gly Tyr  
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25 ttt acg ccc ggt gat ctt agt atc gga tat acc tcg cct tgg gca ggt 144  
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 35 40 45

30 gcc aac tgg ctc aca ttt tac gat gga ggc aag tta gcc gac tac gat 192  
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35 gcc gtc tct tat cct atc ttg cga gag ctg gct cga agc agc ccc gag 240  
 Ala Val Ser Tyr Pro Ile Leu Arg Glu Leu Ala Arg Ser Ser Pro Glu  
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gct gga att cga ctc atc agc caa cgc tcc cat gtt ctc aag cgt gat 288  
 Ala Gly Ile Arg Leu Ile Ser Gln Arg Ser His Val Leu Lys Arg Asp  
 40 85 90 95

ctt cct aaa ctg gaa gtt gcc atg tcg gcc atc tgt caa cgc aat ccc 336  
 Leu Pro Lys Leu Glu Val Ala Met Ser Ala Ile Cys Gln Arg Asn Pro  
 100 105 110

45

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	Arg Ile Val His Asp Asp Val Ala Tyr Leu Val Glu Phe Arg Ser Val	
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10	tgt atc cac acc gga gtc tac ttg aac tgg ctg atg tcc caa tgc tta	480
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15	tcg ctc ggc gcc acg gtg gtt aaa cgt cga gtg aac cat atc aag gat	528
	Ser Leu Gly Ala Thr Val Val Lys Arg Arg Val Asn His Ile Lys Asp	
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25	tgt agt ggt ctc ttt gcc cgg ttc ttg gga ggc gtc gag gac aag aag	624
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35	ttt atg gcc tcc ttt tcc agc act cct gaa aaa gaa aat gaa gac gaa	720
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10 ttt gtt gtc cat aac tat ggt gcc gcc ggt gct ggt tac caa tcc tct 1008  
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15 tac ggc atg gct gat gaa gct gtt tct tac gtc gaa aga gct ctt act 1056  
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25 Phe Met Ala Ser Phe Ser Ser Thr Pro Glu Lys Glu Asn Glu Asp Glu  
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40 Arg Glu Gly Gly Pro Arg Val Glu Leu Glu Lys Ile Pro Gly Val Gly  
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